

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 00:58:38 ; Search time 2074 Seconds
(without alignments)
10968.655 Million cell updates/sec

Title: US-09-308-829-1

Perfect score: 936
Sequence: 1 caacctgactataatg.....gagcttacctctaatta 936

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_hiv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102.2	10.9	1201	9	AL565455
2	91	9.7	1200	13	AL565455
3	87	9.3	1101	29	BX437758
C	87	9.3	1200	13	CNS0039G
					BX415878
					BX415878

5	85.4	9.1	1101	29	CNS00EVL	AL069706	Drosophila
C	6	81.2	8.7	1101	29	CNS0039G	AL063921
C	7	81.2	8.7	1201	9	AL565455	AL565455
C	8	80	8.5	1101	29	CNS00EVL	AL069706
C	9	79.2	8.5	1201	9	AL56104	AL56104
10	78	8.3	1101	29	CNS0021J	AL061936	Drosophila
11	76.8	8.2	1101	29	CNS003BD	AL064091	Drosophila
12	76.4	8.2	994	29	CNS04NOJ	AL298972	Tetradon
13	75.4	8.1	1200	13	BX415878	BX415878	BX415878
14	74.2	7.9	994	13	BX416650	BX416650	BX416650
15	73.2	7.8	1201	13	BX439779	BX439779	BX439779
16	72.6	7.6	836	29	CNS01100	AL099642	Drosophila
17	71.4	7.6	1201	9	AL56104	AL56104	AL56104
18	70.2	7.5	1010	14	CD171719	CD171719	AGENCOURT
C	19	70.2	7.5	1200	13	BX437739	BX437739
C	20	70	7.5	795	29	AG044101	AG044101
C	21	70	7.5	1124	13	BX436282	BX436282
C	22	69.8	7.5	1101	29	CNS00E07	AL069440
C	23	69.6	7.4	1045	13	BX456814	BX456814
C	24	69.6	7.4	1201	13	BX366070	BX366070
C	25	69.4	7.4	1092	29	CNS020K7	AL175696
C	26	69.2	7.4	829	29	CNS03LUB	AL249932
C	27	69.2	7.4	1202	29	CC262481	CC262481
C	28	69	7.4	1008	14	CD329035	CD329035
C	29	68.8	7.4	1200	13	BX437758	BX437758
C	30	68.6	7.3	994	13	BX436885	BX436885
C	31	68.6	7.3	1098	13	BX377526	BX377526
C	32	68.6	7.3	1165	13	BX38369	BX38369
C	33	68.4	7.3	1056	13	BX415058	BX415058
C	34	68.2	7.3	956	13	BX414969	BX414969
C	35	68.2	7.3	1101	29	CNS003DQ	AL064580
C	36	68	7.3	1201	13	BX406288	BX406288
C	37	67.8	7.2	1225	29	CNS0161D	AL106171
C	38	67.4	7.2	1098	13	BX377526	BX377526
C	39	67.2	7.2	939	14	BY720774	BY720774
C	40	67.2	7.2	1201	13	BX360780	BX360780
C	41	67.2	7.2	1201	13	BX461824	BX461824
C	42	67	7.2	928	29	CNS00DKY	AL071865
C	43	66.8	7.1	949	14	CA465606	CA465606
C	44	66.6	7.1	876	29	CNS00991	AL053529
C	45	66.6	7.1	1201	13	BX443774	BX443774

ALIGNMENTS

RESULT 1
AL565455
LOCUS
DEFINITION
AL565455 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS0DP005YO18 3-PRIME, mRNA sequence.

ACCESSION
AL565455
VERSION
AL565455.2 GI:30549492
KEYWORDS
EST.

SOURCE
Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
On Feb 16, 2001 this sequence version replaced gi:12916848.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9232.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DP005BH09NP1&cluster=9232.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :

Db 582 GAKMATTWTTTTCCTTATATWTKRAGATWTTTTTTTWWAAGDMKMTWTTTTTWT 641
 QY 455 TATTTATATCTTATATCTTACACCGGAGACATCTATGAGGATTAAGCCGCTC 514
 Db 642 TTTTTCCTTGTGTTTMMRDKARRAKATKMTTWTWMAWAGAAKRRATWTWMA 701
 QY 515 AAAATATTAAGTAATCATATTAATTTGGAATCTATTTTTCGGAGATCTCAAC 574
 Db 702 AAMWAGAAAGAGAGAGAAATTTTTTTTATKAGARRATWT-----AAMWATATRA 755
 QY 575 AGAATTAATTAACAGATTTCTAGAAAGAGATCTCACTTCCAGGAATTTGACT 634
 Db 756 RCARGADTTTTTATATMTATTTTTTTTWWAAGATKAAAMWMTWTWMAAAAAAT 815
 QY 635 TTAATATCGAATAATCTATGATTAATTAATTAATTAATGAGCTACTTCCCTTATG 644
 Db 816 WMAAGRAAAKATWMAAAAAAAMWMAAAATATATTTTATATAT--AAKARA 872
 QY 695 TAAGCGGAGATTCGCAATTTGACAAAGATGGAACATGACCAATAGACTTATTTG 754
 Db 873 AAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 932
 QY 755 ACTGCAATTAAGAGGACTAGATGATTTTTCGCAATTAATTAATTAATTAATTA 814
 Db 933 WMAAAARAAWMAAAAGAAAGAAWMAAAATTTTTTTTAAATATWMAAAATTTTTT 992
 QY 815 TCAATATGAGACTTATCTATTCATTTGATTTATTTGAAAAATATCTATCATGACA 874
 Db 993 TTTTMAAAAMWMTTTTATWATATWATATAGMAAAATATATATATTAATTAADARA 1052
 QY 875 AAAACCCGCGCAATTAATCTGAGCGTTTGTCTTA 911
 Db 1053 AGAMATATKAGATTAATTTTTTTTTTTTTTTTMA 1089

RESULT 3
 LOCUS CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL063921
 VERSION AL063921.1 GI:4941778
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)
 REFERENCE
 AUTHORS Direct Submission
 TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 JOURNAL - Web : www.genoscope.cns.fr
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila genome project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mosmoser in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's
 p1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 Location/Qualifiers
 1. 1101
 /organism="Drosophila melanogaster"

FEATURES
 source
 1. 1101
 /organism="Drosophila melanogaster"

/mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR08K10"
 /clone_1ib="RPCI-98"
 /note="end : TET3"
 BASE COUNT 201 a 64 c 131 g 202 t 503 others
 ORIGIN
 Query Match 9.3%; Score 87; DB 29; Length 1101;
 Best Local Similarity 18.28; Pred. No. 0.0009;
 Matches 126; Conservative 294; Mismatches 270; Indels 1; Gaps 1;
 QY 34 TAAAACTAAATTAATGATTTTAAATTTCTTAATTAACAGAAATCTGATTTTA 93
 Db 403 WMAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 462
 QY 94 ACTATTAATCTGATTTTATGATTTCTGATGAGATTAATTAATTAAGAGAAAA 153
 Db 463 WTTTATWMAAAAAAATTTTWTTTTATWTTATWTTATWTTTMAAAAAA 522
 QY 154 ATGAAAGATTAATCATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 213
 Db 523 AAAAAMWMAAAATTAATWTTWTTTATTAATTAATTAATTAATTAATTAATTA 582
 QY 214 TATTTGACATGATGACATGATGATGATGATGATGATGATGATGATGATGAT 273
 Db 583 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 642
 QY 274 CTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 333
 Db 643 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 702
 QY 334 ACACACATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 393
 Db 703 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 762
 QY 394 GAAATGCTTATGAGCGCTGCAAAATTAATTAATTAATTAATTAATTAATTAAT 453
 Db 763 AAMMNNAN 822
 QY 454 TTTTATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 512
 Db 823 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 882
 QY 513 TCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 572
 Db 883 HNN 942
 QY 573 ACAGAACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 632
 Db 943 ATMTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1002
 QY 633 CTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 692
 Db 1003 HTWTATWMAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1062
 QY 693 TGTAAAGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 723
 Db 1063 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1093

RESULT 4
 LOCUS BX415878/c 1200 bp mRNA linear EST 15-MAY-2003
 DEFINITION BX415878 Homo sapiens THYMUS Homo sapiens cDNA C50CAP008Y104
 5-PRIME, mRNA sequence.
 ACCESSION BX415878
 VERSION BX415878.1 GI:30765550
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 1200)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr; Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. Contact: Feng Liang Email: fliang@life.com URL:
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID: CS0CAP008BE020P1.
 Location/Qualifiers
 1..1200
 Source

FEATURES
 1..1200
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0CAP008Y104"
 /tissue_type="THYMUS"
 /clone_lib="Homo sapiens THYMUS"
 /note="Vector: pCMVSPORT-6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."
 BASE COUNT
 428 a 70 c 85 g 447 t 170 others

Query Match 9.3%; Score 87; DB 13; Length 1200;
 Best Local Similarity 37.4%; Pred. No. 0.0088;
 Matches 290; Conservative 110; Mismatches 366; Indels 9; Gaps 4;

41 TAAATATTAATCAATTTTAAATTAATTAACAGAAATCGATTTTAACTACTT 100
 1157 WATWKKMTAAATTAATTTTATTTATATWMAAATAATWTAATTTATWTAATA 1098
 101 ACTGATATTCATGATGTCCTGACAGAAATACATTTA-ATTAGAGAAATAATGAA 159
 1097 AAATATTATWATWATWTAATAATTTTAAATATATATWMAAATAATWTAATAAAT 1038
 160 AAGATTAACATCATCAAAATAGTTTTCATTAATTAACAGTACATGATTTCTACTTATTC 219
 1037 AATTTTTTTTTTAMWMAAATAWATWTTTAAWMTWMAATWTTWATWTAATWTA 978
 220 ACCTATCATCAAGAGCTCAAGAGACATTTGCAATGTTAAAGTGAATTAATCTTAT 279
 977 TTTTATWMTWMAAATTTTWTWTTATTTTATTTTAAATAAATAATWTAATAAT 918
 280 GCATTA--CACTATTAAGCTTATGATTAATTAAGATGCGAGGTAATTTTCAAGGACA 336
 917 AAATTAATTAATAAATAAATTTTSTAATTTATTTAATTAATWMAAATTTAAATAA 858
 337 CACACATTAACATGATGATCAAAAATATAGAGGGAAGACATTAATTAATAGTCCGA 396
 857 AATTTTTTTTTTAAATWTTTAAATTAATWMAATTTTAAATTTTAAATTTTGTG 798
 397 ATGCTTATAGAGGCTCTCAAAATTTAAACGAGATGATGATGTTTGGATTA 456
 797 ATTWMAAATAATTTATWTAATWATATTTATGHTATATATATNTATGATTAATW 738
 457 TTTTATATCTTAATTCACACCGGTGATCATCATGAGGAAATTAACGGCTCTGAA 516
 737 TTTCTTATAAATAAATAAATAATTAATTAATTAATTAATTAATTAATTAATTA 678
 517 AATTAATTAAGTAATCAATTAATTAATTTGGAAATCAATTAATTTGGGAAATCAACAG 576
 677 AAATATATWATWTTWTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 618
 577 AACTTAATTAACAGATT--ATTCTAGAAAGATTAATCAATTTCCAGGAATTAATGAC 633
 617 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 558
 634 TTTAAATACAGAAATACCTT-ATGATTAATTAATAAATTTATGAGCTACTTCTCCTT 691

Db 557 TTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 498
 692 ATGTAACGGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
 497 AAATTAATTTTAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 438
 752 TTGACCTACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 806
 437 AAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 383

RESULT 5
 CNS00EVL 1101 bp DNA linear GSS 04-JUN-1999
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:
 DEFINITION BAC29823 of RP11-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL069706 GI:4949849
 GSS.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 I (bases 1 to 1101)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage;
 BP 191 91006 EVRY cedex - FRANCE (E-mail: sequef@genoscope.cns.fr
 - Web: www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazuo Oosawa and
 Aaron Memminger in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RP11-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 P1 and EST libraries. A more detailed description of the BDGP's
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 Location/Qualifiers
 1..1101
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR29823"
 /clone_lib="RP11-98"
 /note="end: 17"
 BASE COUNT
 419 a 91 c 60 g 299 t 232 others

FEATURES
 source
 Query Match 9.1%; Score 85.4; DB 29; Length 1101;
 Best Local Similarity 38.6%; Pred. No. 0.0016;
 Matches 208; Conservative 82; Mismatches 243; Indels 6; Gaps 2;

2 AACCTGACTATTAATGAAGCTGCACTCTTAATAAATAATTAATTAATTAATTA 61
 568 AATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 627
 62 AATTTCTTAATAAAGAGAAATCGATTTTAACTACTGATTTCAATGATTTCTC 121
 628 AATTTTAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 682
 122 GTACGAGTAATACATTTAATTAAGAGAAATAATGAATAATTAATTAATTAAT 181
 683 TWAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 742

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9232.f. For more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF005BH09NP1&cluster=9232.f>. Contact :

Feng Liang Email : liang@lifelab.com URL : http://fulllength.invitrogen.com/Invitrogen_Corporation_1600_Faraday_Avenue_Genoscope_sequence_ID_CS0DF005BH09NP1.

Location/Qualifiers

FEATURES
source

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1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF005Y018"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: PCWSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCWSPORT 6 vector. Library was not normalized."
```

BASE COUNT 550 a 82 c 71 g 313 t 185 others

ORIGIN

Query Match 8.7%; Score 81.2; DB 9; Length 1201;
Best Local Similarity 31.9%; Pred. No. 0.0066;
Matches 257; Conservative 136; Mismatches 411; Indels 1; Gaps 1;

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OY 87 ATTATTACACTGCTACGCTATTTTCAGTATTCGTCAGCGATGTAATCAATTATTAAG 146
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1195 WTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTAT 1136

OY 147 AGAAAAATGAAAAAGATTACATCATCAAAATGTTTCATTAATTCACGACTGAT 206
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DB 1135 WTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTAT 1076

OY 207 TTCTACTTATTCACCTATCAACAGTGCCTTAAGAAACATTTGCAATGTTAAAG 266
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1075 WTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTAT 1016

OY 267 TGATTACTTATTCATACACTATACCTCTTATGATTATTAACATTGCGAGGTAATT 326
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1015 WTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTAT 956

OY 327 TTCAACGACACACATTAAATGATGACTCAAAATATGAGGAAAGACTTTATAT 386
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DB 955 WTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTAT 896

OY 387 TAGTCCGAAATGCTTATGAGGCTCTCAAAATTTAAACGAGATGATCATGATGT 446
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DB 895 WTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTAT 836

OY 447 TTTTGGAATTTATTAATTTCTTATTCACACCGGAGACATCTATGAGAAATTAC 506
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 835 WTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTAT 777

OY 507 GCCTGCTCAAAATATTAAGTAAATCATTAATTTGGAATATTTATTTTGGGAGA 566
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 776 WTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTAT 717

OY 567 ATCTCAACAGACTTAAATAACAGATTATTCGAAAAGAGATTCGTAACCTTCCAGA 626
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 716 WTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTAT 657

OY 627 AATGACTTTAAATTCAGAAATACCTTATGATTAATTTATTAATTTATGACCTACTC 686
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 656 WTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTAT 597

OY 687 TCCATATGTAAGCGGAGAAATTCGACAAAAGATGGGAAACATGAGCAATAGA 746
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 596 WTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTAT 537
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OY 747 CTATTTGACTCACCAATGAGGAGCTAGATGATATTTTCAAAATATAACATAA 806
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DB 536 WTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTAT 477

OY 807 TAGAATTATCAATATGAGAACTTATGCTATTTGCAATTTATCTGAAAAATATTCAT 866
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 476 WTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTAT 417

OY 867 CATACACAAAACCCCGCAGATA 891
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 416 CTTTCTACTTCATGCACTGAGATA 392
```

RESULT 8
CNS00EVL/c
LOCUS DEFINITION
CNS00EVL 1101 bp DNA linear GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPi-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL069706
AL069706.1 GI:4949849
GSS.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr;
Web : www.genoscope.cns.fr)

COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org/TheBDGP/Drosophila_melanogaster_BAC_library
Aaron Mammoler in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPi-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

```
1. 1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29B23"
/clone_lib="RPi-98"
/note="end : 17"
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BASE COUNT 419. a 91 c 60 g 299 t 232 others

ORIGIN

Query Match 8.5%; Score 80; DB 29; Length 1101;
Best Local Similarity 36.6%; Pred. No. 0.01;
Matches 231; Conservative 104; Mismatches 284; Indels 13; Gaps 3;

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OY 44 AATTAATATCATTTATAAATTTCTAAATAACAGAAATCTGATTTTAACACTACT 103
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1099 WTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTATWTAT 1040

OY 104 GCTATTTATCATTTCTGACAGATATCATTTAATTAATTAAGGAAATAAGCAAGA 163
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1039 ATATATTAATTTTAAATAATATATATATATATATATATATATATATATATAT 980

OY 164 TTAACATCAACAAATAGTTTCAATTAATTAACAGTCACTGATTTCTACTTATTCACCT 223
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
```

D	b		979	TATAMATTWMAATAAATWMATMAMTJTAAATAAMAATAVMMMWTMTATTTTTTTT	920
Oy			224	ATCATCAAGTAGCTACTAGAACAACATTCGTAATGTAAAAAGCATTACTTATGCAT	283
D	b		919	TTTWTTTATWMTWTTTATATW-----WTWWAAAAMAWMAATWTATTTTTTATMATYT	865
OY			284	ACACTATACGCCCTTAATGAATATATAAGATTCCAGCGTAAATTTTTCCAACGACACACAT	343
D	b		864	MATITTMATTTTTTTTTTWTATWTTATWTTATWTTATWTTATWTTATWTTATWTTAT--T	808
OY			344	TAAACATTGATCTCAAATAATATNAGGGAAAGACTATATATNTAGTCCGAAATGCTT	403
D	b		807	TATWTTMTWTTWTTATWTTATWTTATWMMMTWMTWAAMWTAATATATMWTAATATWTT	748
OY			404	ATGAGGCCCTCCAAAAATTTAACGACATGATCATGTAGTGTTTGGATTATTTTATA	463
D	b		747	WATWTTWTTTATATWTTTAAWTTATWTTATWATWATWTTWMAWTTTTTTTTTTTTWTA	688
OY			464	TTCTTAATPTCCACACCGGTGATACATCTATNGAGAATATACGCTCTCAAAATATA	523
D	b		687	TTTMAAATTTATTTAAATTTAMWMAAATWMTATTTATAATMA---TTAAATRTTAAA	633
OY			524	AAGTAAATCATAAATATATGGGAATCTATTATTTGGGGAATCTCACAGAATCTAA	583
D	b		632	AATTTTATWMAAAAAATTTTTTTTATATTAATWMAATTTATWATTAATATAMWTTWTA	573
OY			584	ATACAGATATATCTFAGAAAAGATATCGTAACATTTCCAGGAANTTACTTTAAATCA	643
D	b		572	ATTWTTATWATWATWTTTAAATTAATTTTTTTTTTAWTAAAMWTAAMAAATVAMWWW	513
OY			644	GAAATATACCATTATGATATATATATAAATTTAT	675
D	b		512	AAAAAAAAATWMTTTTTTTWATWTAARAATTTWT	481
RESULT 9 AL536104/C AL536104 linear EST 31-MAY-2003					
LOCUS AL536104 Homo sapiens FETL BRAIN Homo sapiens cDNA clone					
DEFINITION CSDDP022YC18 5'-PRIME, mRNA sequence.					
ACCESSION AL536104					
VERSION AL536104.2 GI:31260974					
KEYWORDS EST.					
SOURCE	Homo sapiens	(human)			
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
JOURNAL	L.I.M.B., Gruber,C., Jesse,J. and Polayes,D. Full-length cdna libraries and normalization Unpublished				
COMMENT	On Feb 13, 2001 this sequence version replaced gi:12795957. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by life technologies, a division of Invitrogen. Contact : Feng Liang Email : fliang@life tech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue genoscope sequence ID : CSDF02ZB809OP1. location/Oualifiers 1..1201				
FEATURES	source				

BASE COUNT	vector	Library was not normalized.
ORIGIN	359 a	119 c 146 g 409 t 168 others
Query Match	8.5% ; Score 79.2 ; DB 9 ; Length 1201 ;	
Best Local Similarity	34.5% ; Pred. No. 0.013 ;	
Matches 176 ;	Conservative 99 ; Mismatches 228 ; Indels 7 ; Gaps 1 ;	
QY	50 AATACATTTTAAATTTCTAAATTAACAGAAATCTGATTTTAACTACTGCTATT 109	
Db	1161 WAAATATWHTWTAAMATWTAATATATATCAAMMMWTATWHTATTTTTTTWTMA 1102	
QY	110 TCAATGATATCCGACGAGTAAATCATTTATTAAGAGAAAAATGAAAAAGTTTACA 169	
Db	1101 YMAATATWMTWTTTYYTAAMWAWYMTWTTTAAAMWTATWTAAMATTAAMAAAMWTAW 1042	
QY	170 TCATCAAAATAGTTTCATATTAATTCACGCACTAGTATTTCTACTTATTCACCATCATC 229	
Db	1041 TTTTATATWATASWATWMAAAAMAAAMAAATWATAAWATATTTTWWATTTWTTTAA 982	
QY	230 AAAGTGACTCTAAGAAAGACATTTGCAATGTTAAAGTATTTACTTTATGATACATCA 289	
Db	981 TAAATWTTTAAWMMWMTATTTAYWCMWMTATATATTTTWTWTTWMTATATWATWMMWA 922	
QY	290 TAACCTCTTATGATTTAAAGATTCAGCGGTAATTTTTCACGACACACATTAACA 349	
Db	921 WAAATWMTWTTTAAAMWTTTAAATTAATAAAMWATAAMWT-----AAATTAAMAAATAA 869	
QY	350 TTGATCTCAAAATATATAGAGGAAACATATTTATTTACTTCCGAATGCTTATGAGG 409	
Db	868 ATTTTAAWMAAAATTAAMWATATWMAAAWTTTWTATWTAATTAAMAAAMWTTAAWATTATW 809	
QY	410 CCTCTCAAAATTTAAACGAGATGATCATGATGTTTGGATTTTATTTATTTCTTA 469	
Db	808 ATTAATWMAAAMAAAMWMAAMATATWMTATTAAMWTTTAAATTTAAATATATATWAMA 749	
QY	470 ATTCTCACACCGGTAGTACATCTATGAGGAATTTACCGCTCAAAATTAATTAAGTAA 529	
Db	748 WMTTATATATWMAAMWMAAAATWATTTATATATTTTAAATTAAMWMAAAATTAAMW 689	
QY	530 ATCATTAATTTTGGGAATCTATTTTNTT 559	
Db	688 ATAAWMAATTTATATTAHAHTTATTAAMWH 659	
RESULT 10		
CNS0021J		
LOCUS	1101 bp DNA linear GSS 03-JUN-1999	
DEFINITION	Drosophila melanogaster genome survey sequence TBT3 end of BAC #	
LOCATION	BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit	
FLY)	genomic survey sequence.	
AL061936		
AL061936		
GI:4940214		
VERSION	GSS.	
KEYWORDS	Drosophila melanogaster (fruit fly)	
SOURCE	Drosophila melanogaster	
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
	Ephyridioidae; Drosophilidae; Drosophila.	
REFERENCE	1 (bases 1 to 1101)	
AUTHORS	Genoscope.	
TITLE	Direct Submission	
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage ;	
	Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr	
COMMENT	- Web : www.genoscope.cns.fr)	
	Determination of this BAC-end sequence was carried out as part of a	
	collaboration with the Berkeley Drosophila Genome Project (BDGP).	
	The BDGP is constructing a physical map of the Drosophila	
	melanogaster genome using these BACs. For further information	
	please see http://www.fruitfly.org The BDGP Drosophila	
	melanogaster BAC library was prepared by Kazuo Osoegawa and	
	Aaron Mammeter in Pieter de Jong's laboratory in the Department of	
	Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,	

NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers

1..1101

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone="BACR05N11"

/clone_lib="RPCI-98"

/note="end : TET3"

BASE COUNT 631 a 289 t 146 others

ORIGIN

Query Match 8.3%; Score 78; DB 29; Length 1101;
Best Local Similarity 38.4%; Pred. No. 0.02;
Matches 313; Conservative 65; Mismatches 431; Indels 6; Gaps 1;

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OY 35 AAAAACTAAATATTAATACATTTTAAATTTCTAATAACAGAAATCGATTTTAA 94
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 280 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 339
OY 95 CTACTTACTGCTATTCTATGTTCTGTCAGAGTAATACATTATTAAGAGAAAAA 154
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 340 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 399
OY 155 TGAAGAAGATTACATCAAAATAGTTTCATATTAACATCTACGATTTTCTACTT 214
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 400 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 459
OY 215 ATTTCACCTATCATCAAGTGAAGTCTAAGAAAGACATTCGAATGTTAAAGTATTC 274
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 460 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 519
OY 275 TTTATGCTACCTATTAATCTCTTATGATTAATGAAGTTCAGGTAATTTTCAACA 334
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 520 TTTATTTTATTTTATTAATTAATTTTATTTTATTTTATTTTATTTTAAAWM 579
OY 335 CACACACATTAACATGATCTCAAAATATAGAGGAAGACATTAATTTACTCCG 394
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 580 AATTTTATTAATAAATTTTATTAATTAATAAATAAATAAATAAATAAATAA 639
OY 395 AAATGCTTAATGAGGCTCTCAAAATTTAAACGAGATGATCATGATGTTTGGAT 454
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 640 TTTTWTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 699
OY 455 TATTTTATTTCTTAATTTCTACACCGGTGATCATCTATGAGGAATTAAGCCTGCTC 514
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 700 AATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 759
OY 515 AAAATTAATTAAGTAAATCATTAATTTATGGAATCTTATTTATTTGCGAATCTCAC 574
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 760 TAAATTAATTAAT-----TAAATAATTTTAAATTTTATTTTATTTTAAAAA 813
OY 575 AGAATCTTAATTAACAGATTTATCTAGAAAGATATCGTAATTTCCAGAAATTCGAT 634
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 814 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 873
OY 635 TTTAAATCAGAAATACCTTAATGATTAATTTAAATTTATGAGCTACTCTCTATG 694
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 874 TTTAAATTTTAAATTAATTAATTTATTTTATTTTATTTTATTTTATTTTAAAG 933
OY 695 TTAACGGAGAGAAATGCGACAAAGATGCGAAACATGAGCAATAGACTTATTTG 754
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 934 KTAATKATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 993
OY 755 ACTGACCAATTAAGGAGCTAGATCAGATATTTTTCGAAATTAAGATTAATGAATTA 814
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 994 TAAAGAAATGAAGAAAGTGDATATTTTCKNAATAAATAAATAAATAAATAAAGA 1053

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OY 815 TCAATATGAAGACTTACTGATTTGATATTTAT 849
DB 1054 GAAKAAARAKAADAAGACTTTDAADATATW 1088

RESULT 11

CNS003BD

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
- Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers

1..1101

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone="BACR08K08"

/clone_lib="RPCI-98"

/note="end : TET3"

BASE COUNT 395 a 120 c 103 g 334 t 149 others

ORIGIN

Query Match 8.2%; Score 76.8; DB 29; Length 1101;
Best Local Similarity 40.2%; Pred. No. 0.031;
Matches 212; Conservative 59; Mismatches 254; Indels 3; Gaps 2;

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OY 36 AAACTAAATATTAATACATTTTAAATTTCTAATAATTAACAGAAATCGATTTTAA 95
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 565 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 624
OY 96 TACTTACTGCTATTTCATGTAATTCCTAGACAGTAA--TACATTTAATTAAGAGAAAA 153
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 625 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAAAA 684
OY 154 ATGAAAAAGATTAATCATCAATAATGTTTCAATAATTTACAGTACATGATTTCTACT 213
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 685 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 744
OY 214 TATTTACCTATCATCAAGTACTTAAGAGACATTTGCAATGTTAAAGGATTTA 273
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 745 TATTTTAAAAAATAATTTTATTTTATTTTATTTTATTTTATTTTATTTATTTAA 804
OY 274 CTTTATGCTATCACTATTAATCTCTTATGATTAATTAAGATTTGACGGTAATTTTCAACG 333

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[illegible]

RESULT 12	CNS04NOJ	994 bp	DNA	linear	GSS 01-SEP-2000
LOCUS	CNS04NOJ	994 bp	DNA	linear	GSS 01-SEP-2000
DEFINITION	Tetradon nigroviridis genome survey sequence T7 end of clone 122P04 of library G from Tetradon nigroviridis, genomic survey sequence.				
ACCESSION	AL298972	GI:8037822			
VERSION	AL298972.1	GI:8037822			
KEYWORDS	GSS; genome survey; sequence.				
SOURCE	Tetradon nigroviridis				
ORGANISM	Tetradon nigroviridis				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidae; Tetraodontidae; Tetradon.				
AUTHORS	1 Roest Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fitzmes,C., Wincker,P., Brothier,P., Quetier,F., Saurin,W. and Weissensbach,J. Estimate of human gene number provided by genome-wide analysis using Tetradon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)				
JOURNAL	2				
MEDLINE	Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Costaz,C., Fitzmes,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissensbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis Genome Res. 10 (7), 939-949 (2000)				
PUBMED	10835645				
REFERENCE	3 (bases 1 to 994) Genoscope. Direct Submission Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqdef@genoscope.cns.fr) - Web : www.genoscope.cns.fr This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetradon .				
AUTHORS	1. 994 Location/Qualifiers				
JOURNAL	/organism="Tetradon nigroviridis"				
MEDLINE	/mol_type="genomic DNA"				
PUBMED	/db_xref="taxon:99883"				
REFERENCE	/clone="122P04"				
AUTHORS	/clone.lib="G"				
JOURNAL	/note="Genoscope sequence ID : CORG122DH02LFl-end : T7"				
FEATURES	BASE COUNT 543 a 49 c 36 g 194 t 172 others				
SOURCE	ORIGIN				

Query Match	8.28;	Score 76.4;	DB 29;	Length 994;
Best Local Similarity	43.58;	Pred. No. 0.036;		
Matches 263;	Conservative 25;	Mismatches 306;	Indels 10;	Gaps 2

[illegible]

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